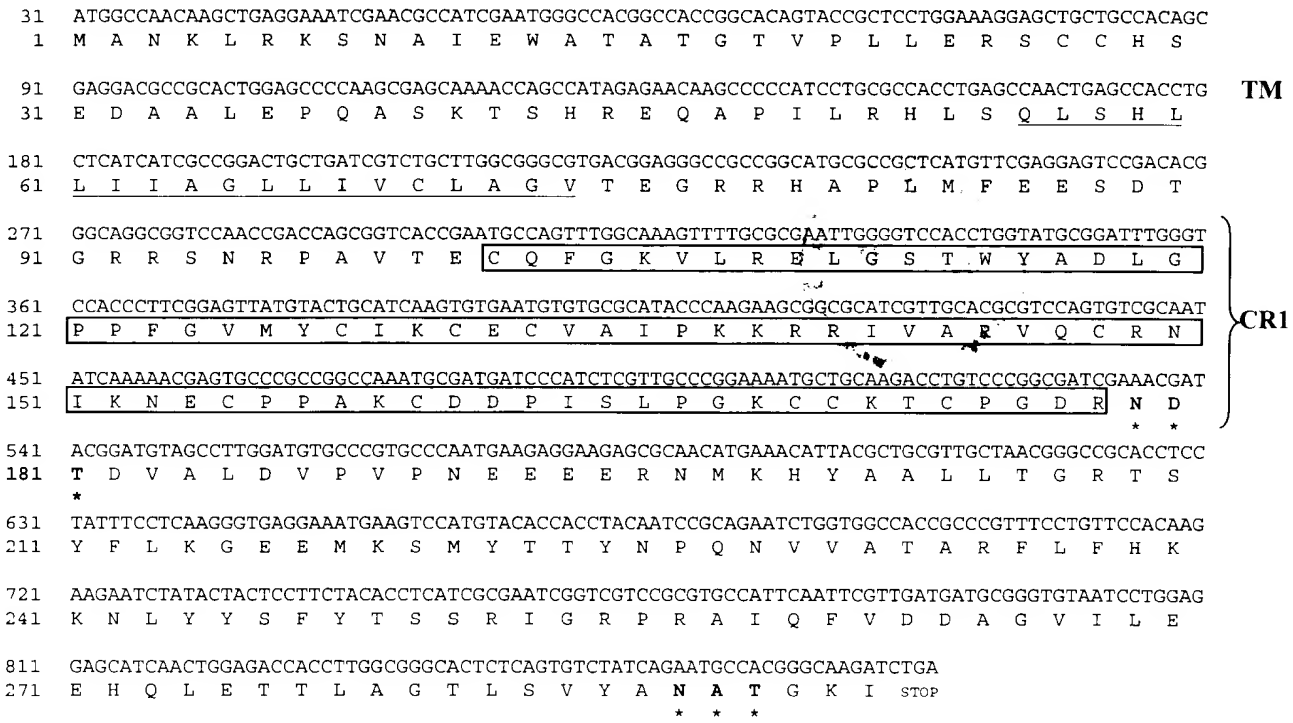
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31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
TM
181 CTCATCATCGCCGGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCCGCCGGCATGCGCCGCTCATGTTCGAGGAGTCCGACACG
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361 CCACCCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTCGCAAT
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CR1
451 ATCAAAAACGAGTGCCCGCCGGCCAAATGCGATGATCCCATCTCGTTGCCCGGAAAATGCTGCAAGACCTGTCCCGGCGATCGAAACGAT
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541 ACGGATGTAGCCTTGGATGTGCCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCCGCACCTCC
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631 TATTTCCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGCAGAATCTGGTGGCCACCGCCCGTTTCCTGTTCCACAAG
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721 AAGAATCTATACTACTCCTTCTACACCTCATCGCGAATCGGTCGTCCGCGTGCCATTCAATTCGTTGATGATGCGGGTGTAATCCTGGAG
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811 GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCTGA
271 E H Q L E T T L A G T L S V Y A N A T G K I STOP

FIGURE 1

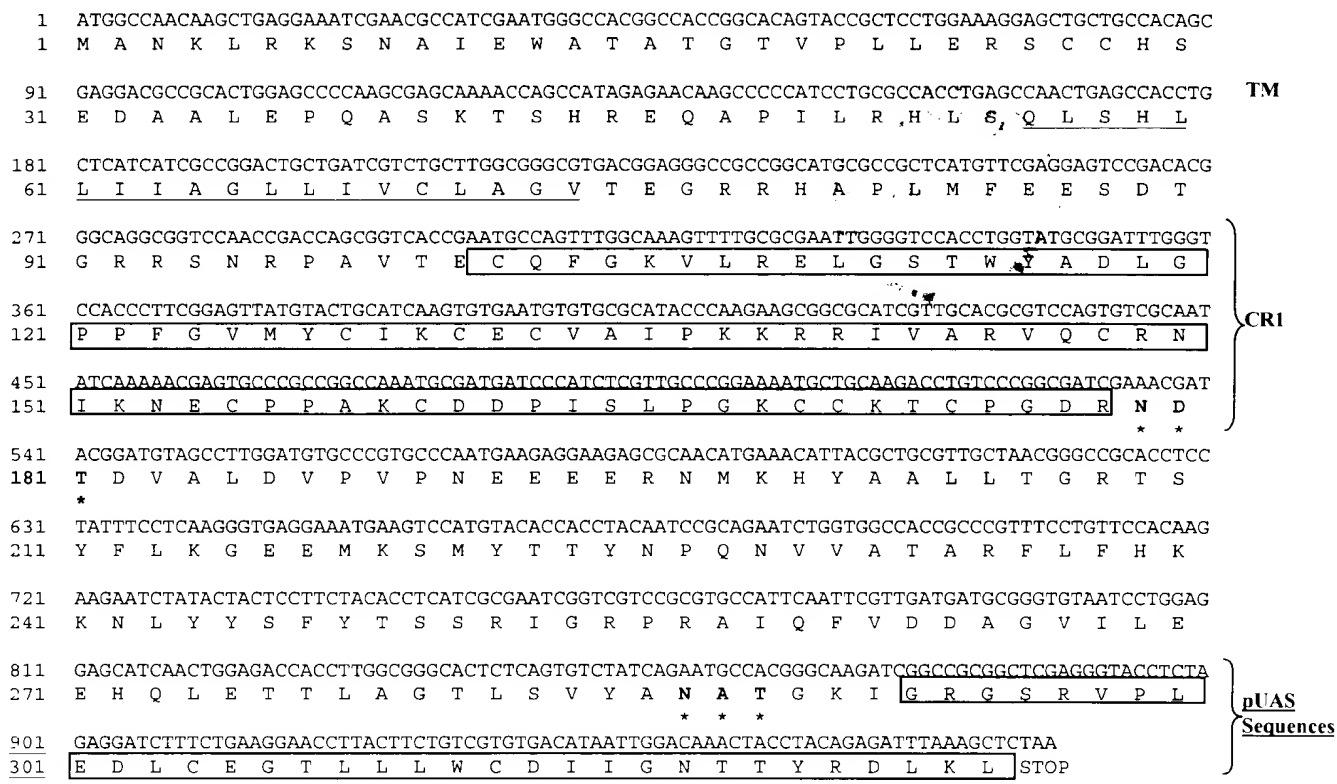
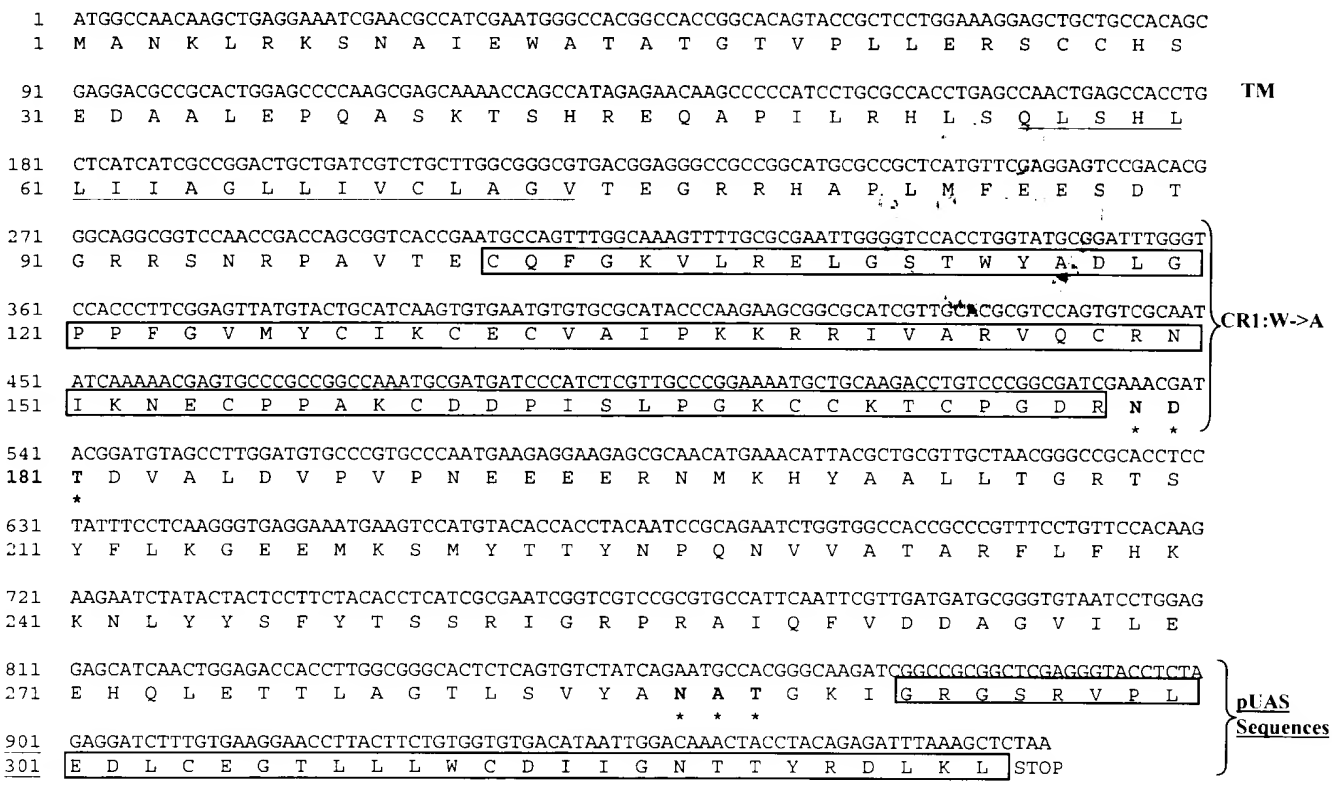


FIGURE 2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91 GAGGACGCCGCACTGGAGCCCCAAGCGAGCAAAACCAGCCATAGAGAACAAGCCCCCATCCTGCGCCACCTGAGCCAACTGAGCCACCTG
31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
TM
181 CTCATCATCGCCGGACTGCTGATCGTCTGCTTGGCGGGCGTGACGGAGGGCCGCCGGCATGCGCCGCTCATGTTCGAGGAGTCCGACACG
61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T
271 GGCAGGCGGTCCAACCGACCAGCGGTCACCGAATGCCAGTTTGGCAAAGTTTTGCGCGAATTGGGGTCCACCTGGTATGCGGATTTGGGT
91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G
361 CCACCCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCCAAGAAGCGGCGCATCGTTGCACGCGTCCAGTGTCGCAAT
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CR1:W->A
451 ATCAAAAACGAGTGCCCGCCGGCCAAATGCGATGATCCCATCTCGTTGCCCGGAAAATGCTGCAAGACCTGTCCCGGCGATCGAAACGAT
151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D
* *
541 ACGGATGTAGCCTTGGATGTGCCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGGCCGCACCTCC
181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S
*
631 TATTTCCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACCTACAATCCGCAGAATCTGGTGGCCACCGCCCGTTTCCTGTTCCACAAG
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721 AAGAATCTATACTACTCCTTCTACACCTCATCGCGAATCGGTCGTCCGCGTGCCATTCAATTCGTTGATGATGCGGGTGTAATCCTGGAG
241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E
811 GAGCATCAACTGGAGACCACCTTGGCGGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCGGCCGCGGCTCGAGGGTACCTCTA
271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L
* * *
pUAS Sequences
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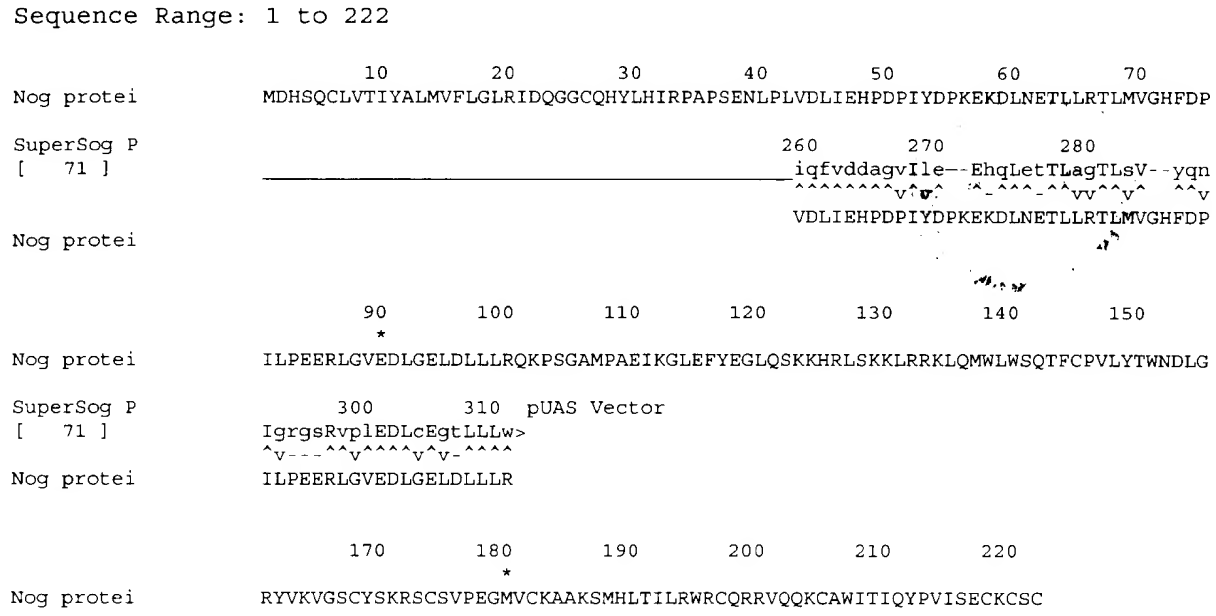
301 E D L C E G T L L L W C D I I G N T T Y R D L K L STOP

FIGURE 3

FIGURE 4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Nog protei
90 100 110 120 130 140 150
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SuperSog P
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FIGURE 5

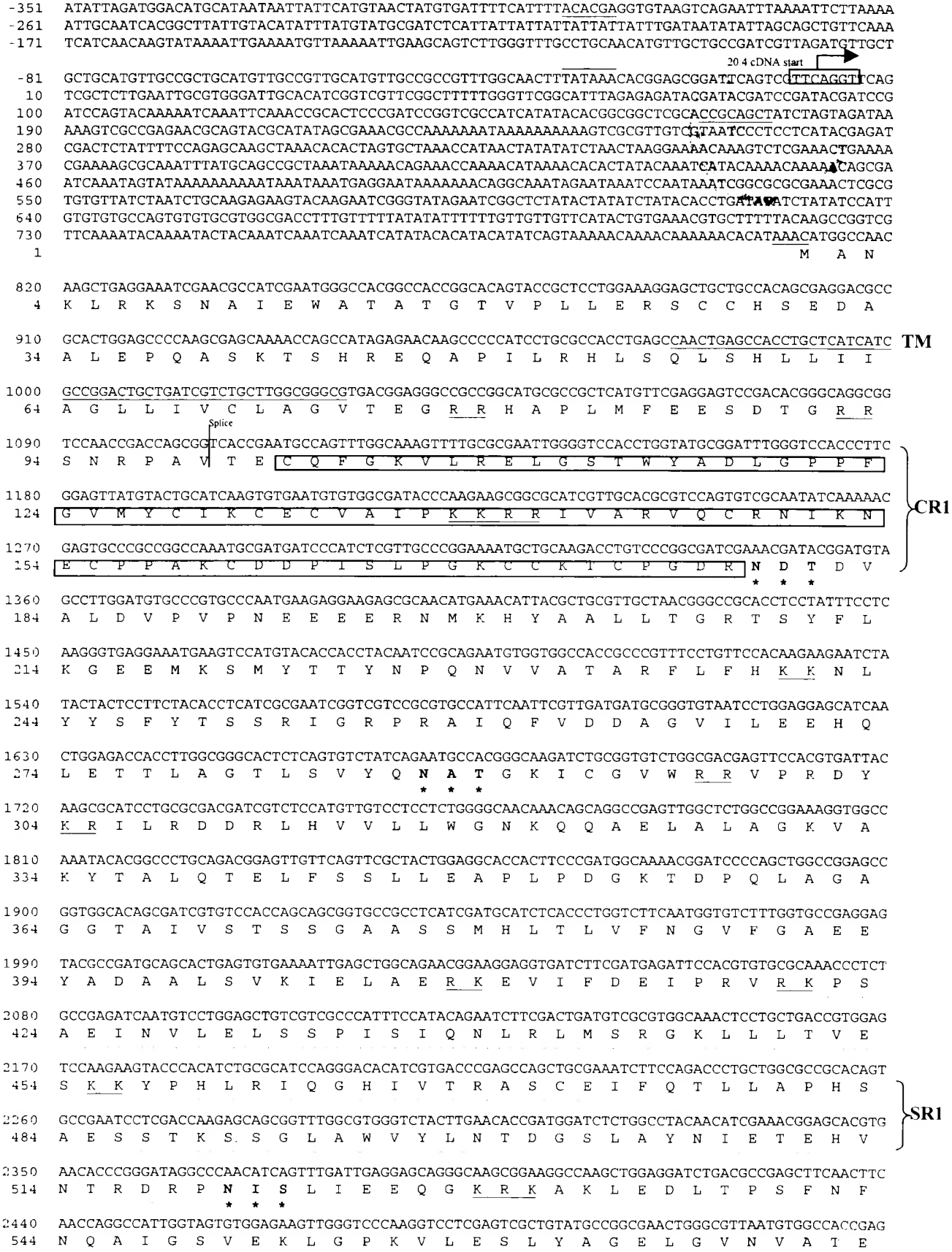

FIGURE 6

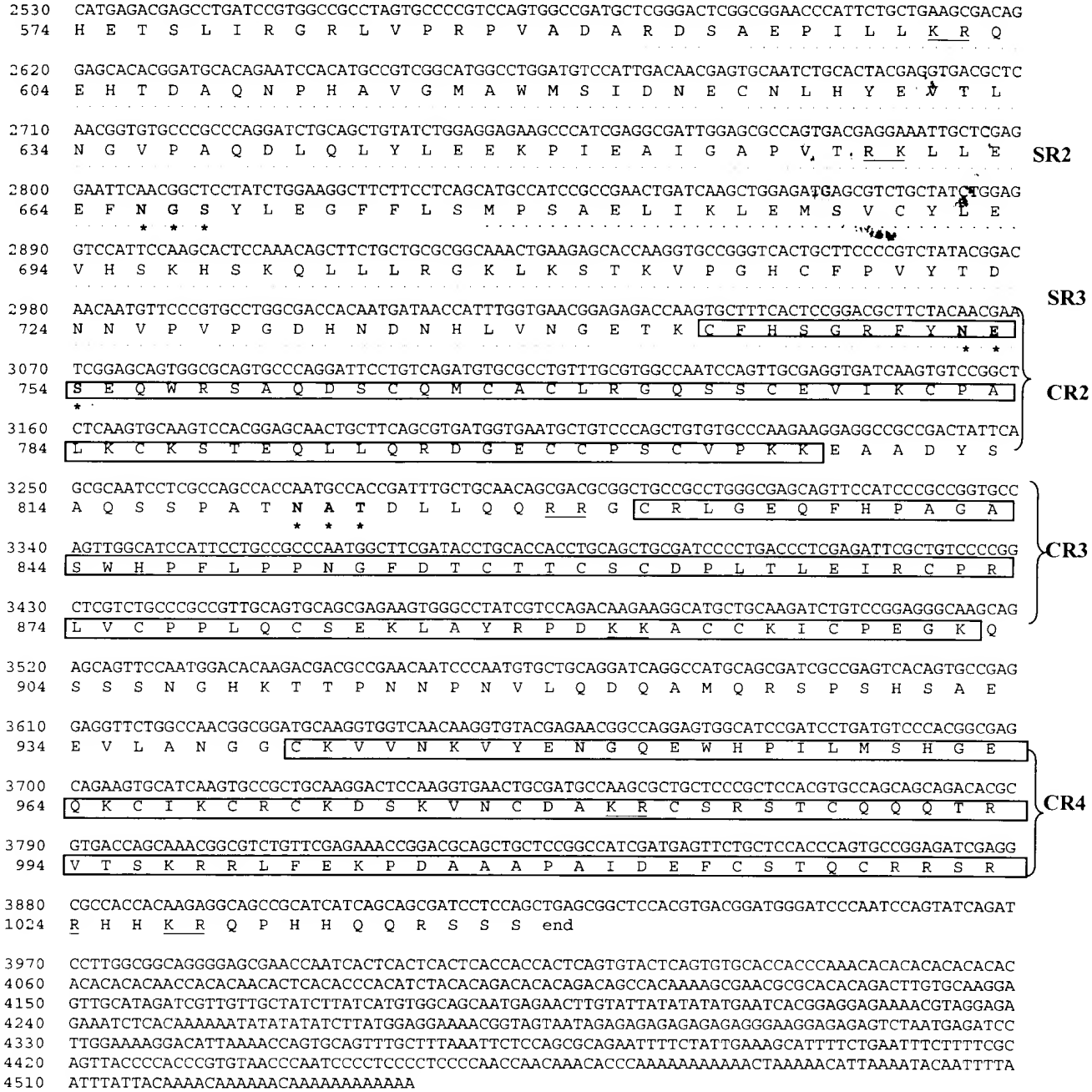

FIGURE 6